Network diffusion models for functional brain connectivity networks

Farras Abdelnour[1], Henning Voss[1], and Ashish Raj[1]
[1]*Radiology, Weill Cornell Medical College, New York, NY, United States*

INTRODUCTION

The relationship between anatomic connectivity of large-scale brain networks and their functional connectivity (FC) is an area of active research. A major goal of brain connectivity research is to discover whether, and how, the structural and functional networks of the brain are related [1]. Strongly connected regions in both networks tend to be grouped similarly [2]. We show that it is possible to develop a realistic network dynamic model. With its simple linearity, such model allows for a closed-form solution which obviates the need for generating simulated signals in order to obtain the relationship between structural and functional networks. We thus present a simple and intuitive network diffusion model which produces an accurate mathematical description of the structure-function relationship. We hypothesize that resting state functional relationships between brain regions result from this *diffusion process* applied to the structural network during rest. We test this hypothesis using healthy structural and functional networks. The network diffusion model applied to the structural networks closely predicts both the spatial and temporal correlation structures seen in the functional networks. We compare our work with published models.

METHOD

In a brain network each node represents a gray matter region located on either the neocortex or in deep brain subcortical areas. First order dynamics of an isolated pair of nodes can be generalized to the entire network with arbitrary topology via the network Laplacian matrix L. Then the entire network is given by $d\mathbf{x}/dt \propto -L\mathbf{x}(t)$. We hypothesize that the configuration at time t of an initial configuration involving only region i is simply the FC of i with all other regions. Therefore we obtain $C_f = \exp(-\beta Lt)$. We hypothesize that at a critical time constant t_{crit}, to be determined experimentally, the network $C_f(t_{crit})$ will match the observed functional network. Linear and nonlinear models of resting-stat connectivity were simulated. All generative models were evaluated by comparing the similarity between the FC predicted by the model and the empirical FC measured from resting state fMRI data.

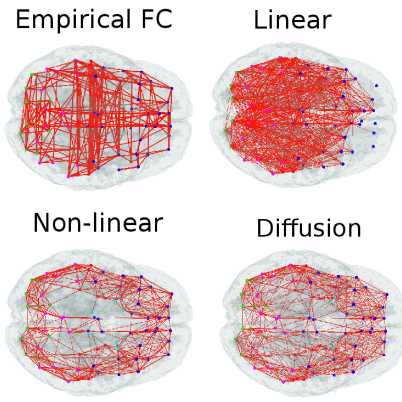

Fig 1: Networks resulting from empirical data, linear model, nonlinear model, and diffusion network.

RESULTS

T1-weighted structural MR and functional fMRI data were collected on 8 healthy adults. Diffusion tractography processing closely followed established pipelines. DPARSF was used for preprocessing of fMRI images. Proposed network diffusion model as well as linear and nonlinear models were simulated. We compare the models' performances by evaluating the Pearson coefficient (PC) of the correlation between each model prediction and the true FC matrix. The proposed network diffusion model provides estimated FC matrix that is better correlated to the true FC matrix than possible with the other models. From Fig 1 the linear model overestimates the network connectivity while the non-linear and proposed models are more accurate. Fig 2 shows functional connectivities due to the linear, nonlinear, and the network diffusion models. The network diffusion model more closely estimates the functional network obtained from empirical FC.

	lFC	nlFC	Network diffusion
Average over 8 subjects	0.3315	0.3630	0.4135
Mean network	0.5306	0.5929	0.6013

Table compares the the average PC over 8 subjects, and the PC for each mean network obtained from the linear model (lFC), the nonlinear model (nlFC), and the network diffusion model. As shown in the table, the proposed method with its simplicity outperforms the current approaches.

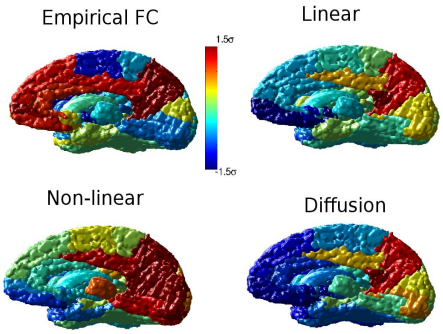

Fig 2: Mean color maps. Clockwise from top left: empirical functional, linear model, the proposed network diffusion functional connectivities, and non-linear model.

CONCLUSION

We show that the covariance structure of BOLD functional brain networks can be captured in a straightforward manner by a simple network diffusion process on the underlying structural brain network. Although previous work has also elucidated this structure-function relationship, our work provides an intuitive and mechanistic explanation for these phenomena, without requiring any details of neural coding or biophysical substrates that sustain them. Our model is completely quantitative, and fully testable. Most importantly, it provides closed form expressions for almost all observed phenomena related to long-range functional activation in the brain.

REFERENCES

[1] C.J. Honey et al.. PNAS , 106(6):2035–2040, 2009. [2] C.J. Honey et al. NeuroImage, 52(3):766–776, 2010.